CLAIMS

1. A method for assaying the presence or the absence of at least one mutation on a strand of nucleic acids paired in a duplex form comprising at least the steps consisting of:

- contacting in a liquid medium said duplex, suspected to include at least one mismatch with at least one compound able to undergo a specific base pairing interaction with said mismatch, said compound being at a concentration of at least 1g/l in said medium and,
- assaying for said mismatch by an analytical method.

2. The method according to claim 1, wherein the strands of nucleic acids paired in duplex form are two DNA strands which are in all or in part complementary.

3. A method for performing Electrophoretic Heteroduplex Analysis "EHDA" on a nucleic acid sample suspected to include at least one heteroduplex, said method comprising at least the steps consisting of:

- contacting in a liquid medium said nucleic acid sample suspected to include at least one heteroduplex, with at least one compound able to undergo a specific base pairing interaction with at least one mismatch of said heteroduplex, said compound being at a concentration of at least 1g/l of said medium,
- assaying for the presence of said heteroduplex thanks to its electrophoretic mobility.

4. The method according to claim 3 comprising a preliminary step of denaturating the nucleic acid sample and renaturating it in conditions convenient to achieve both heteroduplexes and homoduplexes.

5. A method for assaying the presence or the absence of at least one mutation on a single strand of nucleic acid in a liquid medium comprising at least the steps consisting of:

(a) contacting said nucleic acid suspected to include at least one mutation with a nucleic acid probe grafted on a solid support,

(b) allowing the hybridization of at least part of said strand of nucleic acid with the grafted nucleic acid probe,

(c) washing non-hybridized strands, and

(d) assaying for said mutation by an analytical method,

wherein the steps a) and/or c) are performed in the presence of at least one compound able to undergo a specific base pairing interaction with said mutation, said compound being at a concentration of at least 1g/l.

6. The method according to claims 1 to 5 wherein the strand(s) of nucleic acids is a single stranded DNA, RNA, LNA, PNA, or any artificial or natural analog of nucleic acids.

7. The method according to any one of claims 1 to 6, wherein the compound able to undergo a specific base pairing interaction includes at least two groups suitable for hydrogen bonding, in an orientation, polarity and spacing compatible with the creation of attractive interaction with at least one of the bases A, T, G, C and U.

8. The method according to any one of claims 1 to 7, wherein said compound is unable to interfere with polymerisation reactions of nucleotides and/or to be incorporated into a newly polymerized DNA strand.

9. The method according to any one of claims 1 to 8, wherein said compound is one oligonucleotide having a length of less than 5 nucleotides, a nucleoside, a base or a mixture thereof.

10. The method according to claim 9, wherein the oligonucleotide has a length of less than 3 nucleotides and preferably less than 2 nucleotides.

11. The method according to claim 9 or 10, wherein the compound is selected among adenosine, guanosine, uridine, cytidine, thymidine and mixtures thereof.

12. The method according to claim 9, 10 or 11, wherein oligonucleotide(s) or nucleoside(s) in the mixture of oligonucleotides or nucleosides are unable to undergo mutually base pairing interaction.

13. The method according to claim 12, wherein the compound includes cytidine and thymidine or cytidine and adenosine or guanosine and thymidine or guanosine and adenosine.

14. The method according to any one of the claims 1 to 13, wherein the compound(s) is used at a concentration of a least 10 g/l and preferably at least 25 g/l.

15. A method according to any one of claims 1 to 14, in which said compound(s) is in addition bearing at least one substituent.

16. A method according to claim 15, in which said substituent induces in said compound at least one of the following changes:

- increase in solubility,
- change in charge, or
- change in friction with a solvent.

17. The method according to any one of the claims 1 to 16, wherein the mutation to assay is a point mutation.

18. The method according to any one of the claims 1 or 2 and 5 to 17, wherein said mutation is assayed by hybridization assay.

19. The method according to any one of the claims 1 to 4 or 6 to 17, wherein said mutation is assayed by an electrophoretic analysis using a liquid separating medium.

20. The method according to claim 19, wherein said liquid separating medium contains at least a polymer at a concentration of at least 1%, and preferably at least 3% by weight of the total weight of said medium.

21. The method according to claim 19 or 20, wherein said liquid separating medium contains at least a polymer chosen in the group consisting of N,N-disubstituted polyacrylamides and N- substituted polyacrylamides, wherein said N substituents are selected from the group consisting of C_1 to C_{12} alkyl, halo-substituted C_1 to C_{12} alkyl, methoxy-substituted C_1 to C_{12} alkyl, and hydroxyl-substituted C_1 to C_{12} alkyl.

22. The method according to claim 20 or 21, wherein the liquid separation medium contains at least one polymer composed of several polymer segments, said polymer being of the irregular block copolymer type or irregular comb polymer type and having on average at least three junction points established between polymer segments of different chemical or topological nature.

23. The method according to claim 22, wherein the polymer comprises at least one type of polymer segment showing, within the separating medium, specific affinity for the channel wall, and at least one type of polymer segment showing in said medium less or no affinity for the wall.

24. The method according to claim 20 to 23, wherein said polymer contains acrylamide or substituted acrylamides.

25. Use of a method according to any one of the claims 1 to 24 for diagnosing a predisposition to genetic diseases or cancers associated or putatively associated to specific point mutation(s) or the diagnosis or prognosis of said diseases or cancers.

26. Use according to claim 25, wherein said disease is associated to at least a point mutation in a human breast cancer predisposition gene (BRCA).

27. A composition including at least a compound able to undergo specific base pairing interaction at a concentration of at least 1g/l and at least a liquid separating medium.

28. A composition according to claim 27, wherein the compound is as defined in any one of the claims 7 to 16.

29. A composition according to claim 27 or claim 28, wherein said liquid separating medium is a defined in claims 19 to 24.

30. A composition according to any one of claims 27 to 29, wherein said liquid separation medium includes furthermore at least a compound selected among:

- a sieving polymer
- a hydrophilic polymer, and
- a surface-active polymer.

31. A composition including at least a DNA fragment having a nucleic sequence related to a gene on which point mutation(s) has been associated or putatively associated with a disease or an increased predisposition to a disease, and at least a compound able to undergo specific base pairing interaction at a concentration of at least 1g/l, wherein said compound is as defined in anyone of the claims 7 to 16.

32. A composition including at least a compound able to undergo specific base pairing interaction at a concentration of at least 1g/l, and a pair of molecules or groups acting as a DNA probe called "molecular beacon", wherein said compound is as defined in any one of the claims 7 to 16.

33. A kit useful for the screening of a nucleic acid or analog thereof having a sequence related to a gene on which point mutation(s) has been associated or putatively associated with a disease or an increased predisposition to a disease, said kit comprising at least a composition according to any one claims of 27 to 30.

34. A method for assaying a nucleic acid for mutation comprising at least the steps consisting in:

- performing a polymerase chain reaction on said nucleic acid in the presence of at least two primers and a pool of compounds able to undergo specific base pairing interaction with nucleotides or analogue thereof, said compounds being at a combined concentration of at least 1 g/l and being unable to interfere with the polymerase chain reaction and,
- analyzing and/or quantifying the so-obtained DNA fragments.

35. The method according to claim 34, wherein the compound is as defined in any one of the claims 7 to 16.